



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Björck, Lars  
Sjöbring, Ulf

(ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP  
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(C) CITY: Seattle  
(D) STATE: Washington  
(E) COUNTRY: USA  
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/325,278  
(B) FILING DATE: 26-OCT-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: McMasters, David D.  
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(C) REFERENCE/DOCKET NUMBER: 450023.401

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

- (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser  
1 5 10 15

Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser  
20 25 30

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu  
35 40 45

Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr  
50 55 60

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
65 70 75 80

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
85                    90                    95

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
100 105 110

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu  
115 120 125

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
130 135 140

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro  
145 150 155 160

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys  
165 170 175

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu  
180 185 190

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr  
195 200 205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
210 215 220

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
225 230 235 240

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
245 250 255

Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu  
260 265 270

Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr  
275 280 285

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu  
290 295 300

Glu  
305

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 921 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCCAGAAA CTGATTAGA AGAAGAAGTA	60
ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAACCTGCAGA ATTCAAAGGA	120
ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTGAA GAAAGACAAT	180
GGAGAATATA CTGTAGATGT TGCAAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA	240
AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAA CTTAATCTAT	300
GCAGATGGAA AAACACAAAC AGCAGAACATC AAAGGAACAT TTGAAGAAC AACAGCAGAA	360
GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA	420
GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA	480
AAAGAAGAAG TTACTATTAA AGCAAACCTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA	540
GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA	600
GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT	660
AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAG AAGAAGTTAC TATTAAAGCA	720
AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA	780
GCAACAGCAG AAGCATAACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA	840
GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC	900
GAAAAACCAG AAGAATAATA A	921

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser  
1               5                           10                           15

Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser  
20               25                           30

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu  
35               40                           45

Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr  
50               55                           60

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
65               70                           75                           80

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
85               90                           95

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
100              105                           110

Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu  
115              120                           125

Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr  
130              135                           140

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro  
145              150                           155                           160

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys  
165              170                           175

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu  
180              185                           190

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr  
195 200 205

Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly  
210 215 220

Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala  
225 230 235 240

Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly  
245 250 255

Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu  
260 265 270

Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr  
275 280 285

Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu  
290 295 300

Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys  
305 310 315 320

Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val  
325 330 335

Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr  
340 345 350

Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile  
355 360 365

Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile  
370 375 380

Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala  
385 390 395 400

Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val  
405 410 415

Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr  
420 425 430

Glu Met

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli L392/pHDLG, DSM 7055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCCAGAAA CTGATTAGA AGAAGAAGTA	60
ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AACTGCAGA ATTCAAAGGA	120
ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTGAA GAAAGACAAT	180
GGAGAAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA	240
AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAA CTTAATCTAT	300
GCAGATGGAA AAACACAAAC AGCAGAACATT AAAGGAACAT TTGAAGAAC AACAGCAGAA	360
GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA	420
GATAAAGGTT ATACTTTAAA TATTAAATTG GCTGGAAAAG AAAAACACC AGAAGAACCA	480
AAAGAAGAAG TTACTATTAA AGCAAACCTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA	540
GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATT	600
GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT	660

AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA	720
AACTTAATCT ATGCAGATGG AAAAACCTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA	780
GCAACAGCAG AAGCATAACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA	840
GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC	900
GAAAAACCAG AAGAACCCAT GGACACTTAC AAATTAATCC TTAATGGTAA AACATTGAAA	960
GGCGAAACAA CTACTGAAGC TGTTGATGCT GCTACTGCAG AAAAAGTCTT CAAACAATAC	1020
GCTAACGACA ACGGTGTTGA CGGTGAATGG ACTTACGACG ATGCGACTAA GACCTTTACA	1080
GTTACTGAAA ACCAGAAAGT GATCGATGCG TCTGAATTAA CACCAGCCGT GACAACCTTAC	1140
AAACTTGTAA TTAATGGTAA AACATTGAAA GGCAGAAACAA CTACTAAAGC AGTAGACGCA	1200
GAAACTGCAG AAAAAGCCTT CAAACAATAC GCTAACGACA ACGGTGTTGA TGGTGTTGG	1260
ACTTATGATG ATGCGACTAA GACCTTTACG GTAACTGAAA TGTAATAA	1308

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC	48
Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn	
1 5 10 15	

AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu	20	25	30	96
AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys	35	40	45	144
AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg	50	55	60	192
AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu	65	70	75	240
GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu	85	90	95	288
GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg	100	105	110	336
GAC TAC CAT AGA GCT ACC GCT TTA GAA AAA GAG TTA GAA GAG AAA AAG Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Glu Lys Lys	115	120	125	384
AAA GCT CTT GAA TTA GCG ATA GAC CAA GCG AGT CAG GAC TAT AAT AGA Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg	130	135	140	432
GCT AAC GTC TTA GAA AAA GAG TTA GAA ACG ATT ACT AGA GAA CAA GAG Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu	145	150	155	480
ATT AAT CGT AAT CTT TTA GGC AAT GCA AAA CTT GAA CTT GAT CAA CTT Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu	165	170	175	528
TCA TCT GAA AAA GAG CAG CTA ACG ATC GAA AAA GCA AAA CTT GAG GAA Ser Ser Glu Lys Glu Gln Leu Thr Ile Glu Lys Ala Lys Leu Glu Glu	180	185	190	576

GAA AAA CAA ATC TCA GAC GCA AGT CGT CAA AGC CTT CGT CGT GAC TTG Gl <sub>u</sub> Lys Gl <sub>n</sub> Ile Ser Asp Ala Ser Arg Gl <sub>n</sub> Ser Leu Arg Arg Asp Leu 195 200 205	624
GAC GCA TCA CGT GAA GCT AAG AAA CAG GTT GAA AAA GAT TTA GCA AAC Asp Ala Ser Arg Gl <sub>u</sub> Ala Lys Lys Gl <sub>n</sub> Val Gl <sub>u</sub> Lys Asp Leu Ala Asn 210 215 220	672
TTG ACT GCT GAA CTT GAT AAG GTT AAA GAA GAC AAA CAA ATC TCA GAC Leu Thr Ala Gl <sub>u</sub> Leu Asp Lys Val Lys Gl <sub>u</sub> Asp Lys Gl <sub>n</sub> Ile Ser Asp 225 230 235 240	720
GCA AGC CGT CAA CGG CTT CGC CGT GAC TTG GAC GCA TCA CGT GAA GCT Ala Ser Arg Gl <sub>n</sub> Arg Leu Arg Asp Leu Asp Ala Ser Arg Gl <sub>u</sub> Ala 245 250 255	768
AAG AAA CAG GTT GAA AAA GAT TTA GCA AAC TTG ACT GCT GAA CTT GAT Lys Lys Gl <sub>n</sub> Val Gl <sub>u</sub> Lys Asp Leu Ala Asn Leu Thr Ala Gl <sub>u</sub> Leu Asp 260 265 270	816
AAG GTT AAA GAA GAA AAA CAA ATC TCA GAC GCA AGC CGT CAA CGG CTT Lys Val Lys Gl <sub>u</sub> Gl <sub>u</sub> Lys Gl <sub>n</sub> Ile Ser Asp Ala Ser Arg Gl <sub>n</sub> Arg Leu 275 280 285	864
CGC CGT GAC TTG GAC GCA TCA CGT GAA GCT AAG AAA CAA GTT GAA AAA Arg Arg Asp Leu Asp Ala Ser Arg Gl <sub>u</sub> Ala Lys Lys Gl <sub>n</sub> Val Gl <sub>u</sub> Lys 290 295 300	912
GCT TTA GAA GAA GCA AAC AGC AAA TTA GCT GCT CTT GAA AAA CTT AAC Ala Leu Gl <sub>u</sub> Gl <sub>u</sub> Ala Asn Ser Lys Leu Ala Ala Leu Gl <sub>u</sub> Lys Leu Asn 305 310 315 320	960
AAA GAG CTT GAA GAA AGC AAG AAA TTA ACA GAA AAA GAA AAA GCT GAA Lys Gl <sub>u</sub> Leu Gl <sub>u</sub> Gl <sub>u</sub> Ser Lys Lys Leu Thr Gl <sub>u</sub> Lys Gl <sub>u</sub> Lys Ala Gl <sub>u</sub> 325 330 335	1008
CTA CAA GCA AAA CTT GAA GCA GAA GCA AAA GCA CTC AAA GAA CAA TTA Leu Gl <sub>n</sub> Ala Lys Leu Gl <sub>u</sub> Ala Gl <sub>u</sub> Ala Lys Ala Leu Lys Gl <sub>u</sub> Gl <sub>n</sub> Leu 340 345 350	1056
GCG AAA CAA GCT GAA GAA CTC GCA AAA CTA AGA GCT GGA AAA GCA TCA Ala Lys Gl <sub>n</sub> Ala Gl <sub>u</sub> Gl <sub>u</sub> Leu Ala Lys Leu Arg Ala Gl <sub>y</sub> Lys Ala Ser 355 360 365	1104
GAC TCA CAA ACC CCT GAT ACA AAA CCA GGA AAC AAA GCT CTT CCA GGT	1152

Asp Ser Gln Thr Pro Asp Thr Lys Pro Gly Asn Lys Val Leu Pro Gly			
370	375	380	
AAA GGT CAA GCA CCA CAA GCA GGT ACA AAA CCT AAC CAA AAC AAA GCA			1200
Lys Gly Gln Ala Pro Gln Ala Gly Thr Lys Pro Asn Gln Asn Lys Ala			
385	390	395	400
CCA ATG AAG GAA ACT AAG AGA CAG TTA CCA TCA ACA GGT GAA ACA GCT			1248
Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala			
405	410	415	
AAC CCA TTC TTC ACA GCG GCA CGC GTT ACT GTT ATG GCA ACA GCT GGA			1296
Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly			
420	425	430	
GTA GCA GCA GTT GTA AAA CGC AAA GAA GAA AAC TAA			1332
Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn			
435	440		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn			
1	5	10	15
Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu			
20	25	30	
Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys			
35	40	45	
Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg			
50	55	60	
Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu			
65	70	75	80

Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu  
85 90 95

Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg  
100 105 110

Asp Tyr His Arg Ala Thr Ala Leu Glu Lys Glu Leu Glu Glu Lys Lys  
115 120 125

Lys Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Gln Asp Tyr Asn Arg  
130 135 140

Ala Asn Val Leu Glu Lys Glu Leu Glu Thr Ile Thr Arg Glu Gln Glu  
145 150 155 160

Ile Asn Arg Asn Leu Leu Gly Asn Ala Lys Leu Glu Leu Asp Gln Leu  
165 170 175

Ser Ser Glu Lys Glu Gln Leu Thr Ile Glu Lys Ala Lys Leu Glu Glu  
180 185 190

Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Ser Leu Arg Arg Asp Leu  
195 200 205

Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys Asp Leu Ala Asn  
210 215 220

Leu Thr Ala Glu Leu Asp Lys Val Lys Glu Asp Lys Gln Ile Ser Asp  
225 230 235 240

Ala Ser Arg Gln Arg Leu Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala  
245 250 255

Lys Lys Gln Val Glu Lys Asp Leu Ala Asn Leu Thr Ala Glu Leu Asp  
260 265 270

Lys Val Lys Glu Glu Lys Gln Ile Ser Asp Ala Ser Arg Gln Arg Leu  
275 280 285

Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys  
290 295 300

Ala Leu Glu Glu Ala Asn Ser Lys Leu Ala Ala Leu Glu Lys Leu Asn  
305 310 315 320

Lys Glu Leu Glu Glu Ser Lys Lys Leu Thr Glu Lys Glu Lys Ala Glu  
325 330 335

Leu Gln Ala Lys Leu Glu Ala Glu Ala Lys Ala Leu Lys Glu Gln Leu  
340 345 350

Ala Lys Gln Ala Glu Glu Leu Ala Lys Leu Arg Ala Gly Lys Ala Ser  
355 360 365

Asp Ser Gln Thr Pro Asp Thr Lys Pro Gly Asn Lys Ala Val Pro Gly  
370 375 380

Lys Gly Gln Ala Pro Gln Ala Gly Thr Lys Pro Asn Gln Asn Lys Ala  
385 390 395 400

Pro Met Lys Glu Thr Lys Arg Gln Leu Pro Ser Thr Gly Glu Thr Ala  
405 410 415

Asn Pro Phe Phe Thr Ala Ala Arg Val Thr Val Met Ala Thr Ala Gly  
420 425 430

Val Ala Ala Val Val Lys Arg Lys Glu Glu Asn  
435 440

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTCAGGCGG CGCCGGTAGA AAATAAAGAA GAAACACCAG AAAC 44

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Glu Asn Lys Glu Glu Thr Pro Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCAGCAGG ATTCTTATTA TTCTTCTGGT TTTTCGTCAA CTTTCTT

47

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGCAGCAGC CATGGGTTCT TCTGGTTTT CGTCAACTTT CTTA

44

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCATGGAC ACTTACAAAT TAATCCTTAA TG GT

34

(2) INFORMATION FOR SEQ ID NO:12:

- Sub H: >*
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly  
1                5                              10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAGGTCGACT TATTACATTT CAGTTACCGT AAAGGTCTTA GT

42

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

*Sub 4)*  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGCTTAAGG AGGTTAACG ATGAAAAAAA CTGCTATCGC TATCGCTGTT GCTCTGGCTG

60

GTTTCGCTAC TGTTGCTCAG GCGGCGCCGA GATCTAAACA GGAATTCGAG CTCGGTACCC

120

GGGGATCCTC TAGAGCTGAC CTGCAGGCAT GC

152